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- (2) INFORMATION FOR SEQ ID NO:1:

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 137..1766

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAAGTGATG	CCACTTGGTT	AAGGTCCCAG	AGCAGGTCAG	AATCAGACCT	AGGATCAGAA	60
ACCTGGCTCC	TGGCTCCTGG	CTCCCTACTC	TTCTAAGGAT	CGCTGTCCTG	ACAGAAGAGA	120
ACTCCTCTTT	CCTAAA	ATG GAG TCG AGT AAA AAG ATG GAC TCT CCT GGC				169
		Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly				
	1		5		10	
GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG CAC ACT GAC CGC AGT GCT						217
Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala						
	15		20		25	

GGG	ACG	CCA	GTT	T	TC	CCT	GAA	CAA	GGA	GGT	TAC	AA	AA	AAG	TTT	265
Gly	Thr	Pro	Val	P	al	Pro	Glu	Gln	Gly	Gly	Tyr	Leu	Leu	Lys	Phe	
		30					35					40				
GTG	AAG	ACC	GTG	GAG	GAC	AAG	TAC	AAG	TGT	GAG	AAG	TGC	CAC	CTG	GTG	313
Val	Lys	Thr	Val	Glu	Asp	Lys	Tyr	Lys	Cys	Glu	Lys	Cys	His	Leu	Val	
	45					50					55					
CTG	TGC	AGC	CCG	AAG	CAG	ACC	GAG	TGT	GGG	CAC	CGC	TCC	TGC	GAG	AGC	361
Leu	Cys	Ser	Pro	Lys	Gln	Thr	Glu	Cys	Gly	His	Arg	Ser	Cys	Glu	Ser	
	60				65					70					75	
TGC	ATG	GCG	GCC	CTG	CTG	AGC	TCT	TCA	AGT	CCA	AAA	TGT	ACA	GCG	TGT	409
Cys	Met	Ala	Ala	Leu	Leu	Ser	Ser	Ser	Ser	Pro	Lys	Cys	Thr	Ala	Cys	
				80					85					90		
CAA	GAG	AGC	ATC	GTT	AAA	GAT	AAG	GTG	TTT	AAG	GAT	AAT	TGC	TGC	AAG	457
Gln	Glu	Ser	Ile	Val	Lys	Asp	Lys	Val	Phe	Lys	Asp	Asn	Cys	Cys	Lys	
			95					100					105			
AGA	GAA	ATT	CTG	GCT	CTT	CAG	ATC	TAT	TGT	CGG	AAT	GAA	AGC	AGA	GGT	505
Arg	Glu	Ile	Leu	Ala	Leu	Gln	Ile	Tyr	Cys	Arg	Asn	Glu	Ser	Arg	Gly	
		110					115					120				
TGT	GCA	GAG	CAG	TTA	ACG	CTG	GGA	CAT	CTG	CTG	GTG	CAT	TTA	AAA	AAT	553
Cys	Ala	Glu	Gln	Leu	Thr	Leu	Gly	His	Leu	Leu	Val	His	Leu	Lys	Asn	
	125					130					135					
GAT	TGC	CAT	TTT	GAA	GAA	CTT	CCA	TGT	GTG	CGT	CCT	GAC	TGC	AAA	GAA	601
Asp	Cys	His	Phe	Glu	Glu	Leu	Pro	Cys	Val	Arg	Pro	Asp	Cys	Lys	Glu	
	140				145					150					155	
AAG	GTC	TTG	AGG	AAA	GAC	CTG	CGA	GAC	CAC	GTG	GAG	AAG	GCG	TGT	AAA	649
Lys	Val	Leu	Arg	Lys	Asp	Leu	Arg	Asp	His	Val	Glu	Lys	Ala	Cys	Lys	
				160				165					170			
TAC	CGG	GAA	GCC	ACA	TGC	AGC	CAC	TGC	AAG	AGT	CAG	GTT	CCG	ATG	ATC	697
Tyr	Arg	Glu	Ala	Thr	Cys	Ser	His	Cys	Lys	Ser	Gln	Val	Pro	Met	Ile	
			175					180					185			
GCG	CTG	CAG	AAA	CAC	GAA	GAC	ACC	GAC	TGT	CCC	TGC	GTG	GTG	GTG	TCC	745
Ala	Leu	Gln	Lys	His	Glu	Asp	Thr	Asp	Cys	Pro	Cys	Val	Val	Val	Ser	
		190					195					200				
TGC	CCT	CAC	AAG	TGC	AGC	GTC	CAG	ACT	CTC	CTG	AGG	AGC	GAG	GGG	ACA	793
Cys	Pro	His	Lys	Cys	Ser	Val	Gln	Thr	Leu	Leu	Arg	Ser	Glu	Gly	Thr	
	205					210					215					
AAC	CAG	CAG	ATC	AAG	GCC	CAC	GAG	GCC	AGC	TCC	GCC	GTG	CAG	CAC	GTC	841
Asn	Gln	Gln	Ile	Lys	Ala	His	Glu	Ala	Ser	Ser	Ala	Val	Gln	His	Val	
	220				225					230					235	
AAC	CTG	CTG	AAG	GAG	TGG	AGC	AAC	TCG	CTC	GAA	AAG	AAG	GTT	TCC	TTG	889
Asn	Leu	Leu	Lys	Glu	Trp	Ser	Asn	Ser	Leu	Glu	Lys	Lys	Val	Ser	Leu	
				240					245					250		
TTG	CAG	AAT	GAA	AGT	GTA	GAA	AAA	AAC	AAG	AGC	ATA	CAA	AGT	TTG	CAC	937
Leu	Gln	Asn	Glu	Ser	Val	Glu	Lys	Asn	Lys	Ser	Ile	Gln	Ser	Leu	His	
			255					260					265			
AAT	CAG	ATA	TGT	AGC	TTT	GAA	ATT	GAA	ATT	GAG	AGA	CAA	AAG	GAA	ATG	985
Asn	Gln	Ile	Cys	Ser	Phe	Glu	Ile	Glu	Ile	Glu	Arg	Gln	Lys	Glu	Met	
		270					275					280				
CTT	CGA	AAT	AAT	GAA	TCC	AAA	ATC	CTT	CAT	TTA	CAG	CGA	GTG	ATA	GAC	1033
Leu	Arg	Asn	Asn	Glu	Ser	Lys	Ile	Leu	His	Leu	Gln	Arg	Val	Ile	Asp	
	285					290					295					

Protein Data Bank

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CACCTGACAC GTTTTAT T AGACTAGCCA CACTTCACTC TGAAGA A TTTATCCTTC 1986
 AACAAAGCATA AATATTG G TCAGAGAAGG TTTTCATTTT CATTTTAA GATCTAGTTA 2046
 ATTAAGGTGG AAAACATATA TGCTAAACAA AAGAAACATG ATTTTCTTC CTAAACTTG 2106
 AACACCAAAA AACACACACA CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT 2166
 AAGTAAAAGG AGAATTTATG AAATAGTAAT GCAATTCTGA TATCTTCTTT CTAAATTC A 2226
 AGAGTGCAAT TTTG 2240

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 543 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
 1 5 10 15
 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
 20 25 30
 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
 35 40 45
 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
 50 55 60
 Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser Cys Met Ala Ala Leu
 65 70 75 80
 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
 85 90 95
 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
 100 105 110
 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
 115 120 125
 Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
 130 135 140
 Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
 145 150 155 160
 Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
 165 170 175
 Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
 180 185 190
 Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
 195 200 205
 Ser Val Gln Thr Leu Leu Arg Ser Glu Gly Thr Asn Gln Gln Ile Lys
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Ala His Glu Ala S er Ala Val Gln His Val Asn Leu Lys Glu
 225 30 235 240
 Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser
 245 250 255
 Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser
 260 265 270
 Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu
 275 280 285
 Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys
 290 295 300
 Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe Arg Gln Asn Trp Glu
 305 310 315 320
 Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val
 325 330 335
 Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn
 340 345 350
 Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser
 355 360 365
 Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Arg Phe Gln Val Leu
 370 375 380
 Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr
 385 390 395 400
 Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr
 405 410 415
 Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
 420 425 430
 Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
 435 440 445
 Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro
 450 455 460
 Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg
 465 470 475 480
 Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe
 485 490 495
 Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe
 500 505 510
 Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr
 515 520 525
 Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
 530 535 540

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCAAA AAGGTGGCCA AG

22

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGATCATCAC TGTCTCTCCT GCAC

24

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAATTCAAG GCCCCCACC CCAAG

25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGATCAACTC TCTTTGCCAT CCTC

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCAAG AGAAAGGAAG TACAG

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGATCACTA GACCAAGCTT TGGAT

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAATTCAAA AAGAAGCCCT TGTGCCT

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTCGACTTA ACTGGGCTTC ATCCCA

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGTTAACTG CTCTGCACAA

20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTACATTTTG GACTTGAAGA

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCCCGG GGATCCGTCG ACCTGCAG

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